AMENDMENTS TO THE CLAIMS

1. (Currently amended)   A system for ~~designing a~~ determining a location of a target sequence in a genome sequence~~probes using heterogeneous genetic information~~, comprising:

a storage unit storing a crosslink map, wherein the crosslink map comprises a record for a sequence information for each version of a genome sequence comprising the sequence information ~~having records according to the version of a genome sequence~~;

an information search unit, for searching for ~~the~~ identifier information and sequence information corresponding to a target ~~genetic information~~sequence among the ~~genetic information about the genome sequence~~records in the crosslink map; and

a location estimation unit, for determining a reference group ~~made up of~~comprising reference ~~genetic~~sequence information for an organism, wherein the reference sequence information is represented in the crosslink map by ~~which is contained in~~more than a predetermined number ~~in an organism~~of records, calculating a difference ~~values~~ of ~~the~~a start positions and ~~the~~an end positions of ~~the~~a reference ~~genetic~~sequence information ~~based on~~obtained from the crosslink map, and determining ~~the~~a location of the target ~~genetic information~~sequence ~~on~~in ~~the latest~~a genome sequence by a location shift corresponding to the difference values.

2. (Currently amended)   The system of claim 1, further comprising
an information integration unit, for receiving genome sequence data ~~corresponding to entries recorded on the crosslink map~~from various sources ~~about the genome sequence~~and transforming the received data into data formats recognized by the crosslink map.

3. (Currently amended)   The system of claim 1, wherein ~~entries recorded~~a record for a sequence information ~~in~~on the crosslink map comprises
a name of ~~the~~a genome sequence,
a version of the genome sequence,
an identifier of a ~~genetic~~sequence information ~~about~~in the genome sequence,
a start position and an end position of the ~~genetic~~sequence information ~~on~~in the genome sequence, and
a length of the ~~genetic~~sequence information ~~about~~in the genome sequence.

4. (Currently amended)   The system of claim 1, wherein the location estimation unit determines the location of the target ~~genetic information~~sequence by assigning a higher priority to the calculated difference values ~~calculated with respect to genetic~~for a reference sequence information ~~which is contained in a more number in an organism~~represented in the crosslink map by a larger number of records.

5. (Currently amended)   The system of claim 1, wherein the location estimation unit comprises:

an estimation region setting portion for calculating a difference ~~values~~ of ~~the~~a start ~~positions~~ and ~~the~~an end ~~positions~~ of ~~genetic~~sequence information in the crosslink map excluded from the reference group ~~based on the crosslink map~~ and setting an estimation region for the location of the target ~~genetic information~~sequence ~~on~~in the ~~latest~~genome sequence based on the calculated difference values; and

a location determining portion for determining the location of the target ~~genetic information~~sequence in the estimation region of the ~~latest~~genome sequence by a location shift corresponding to the calculated difference ~~values~~ ~~calculated with respect to~~for the reference ~~genetic~~ sequence information.

6. (Currently amended)   The system of claim 1, wherein the location estimation unit further comprises

an updating portion for updating the reference group ~~in such a way to~~, ~~calculate~~calculating a difference ~~values~~ of ~~the~~a start ~~positions~~ and ~~the~~an end ~~positions~~ ~~of~~for each sequence ~~genetic~~ information ~~which is commonly present on individual versions of the genome sequence~~in the updated reference group, and selecting ~~genetic~~sequence information in which the calculated difference ~~values~~ ~~are~~is within a predetermined range.

7. (Currently amended)   A method of ~~designing a~~ determining a location of a target~~probes~~ sequence ~~using~~ in a genome sequence~~heterogeneous genetic information~~, the method comprising:

inputting a target sequence;

~~creating a crosslink map having records according to the version of a genome sequence;~~

searching for ~~the~~ identifier information and sequence information corresponding to the target ~~genetic information~~sequence ~~among the genetic information about the genome sequence~~ in ~~the~~ a crosslink map,

wherein the crosslink map comprises a record for a sequence information for each version of a genome sequence comprising the sequence information;

determining a reference group ~~made up of~~comprising reference ~~genetic~~sequence information, wherein the reference sequence information for an organism ~~which~~ is ~~contained~~represented in the crosslink map ~~in~~by more than a predetermined number ~~in an organism~~of records;

calculating a difference values of ~~the~~a start positions and ~~the~~an end positions of ~~the~~a reference ~~genetic~~sequence information ~~based on~~obtained from the crosslink map; and

determining ~~the~~a location of the target ~~genetic information~~sequence ~~on~~in the ~~latest~~a genome sequence by a location shift corresponding to the difference values.

8. (Currently amended)   The method of claim 7, wherein ~~entries~~a record for a sequence information recorded ~~on~~in the crosslink map comprises

a name of ~~the~~a genome sequence,

a version of the genome sequence,

an identifier ~~of~~for ~~the~~a ~~genetic~~sequence information ~~about~~in the genome sequence,

a start position and an end position of the ~~genetic~~sequence information ~~on~~in the genome sequence, and

a length of the ~~genetic~~sequence information ~~about~~in the genome sequence.

9. (Currently amended)   The method of claim 7, wherein determining the location of the target ~~genetic information~~sequence is carried out by

assigning a higher priority to the difference values calculated ~~with respect to~~for ~~genetic~~a reference sequence information ~~which is~~represented ~~contained in a more number in an organism~~in the crosslink map by a larger number of records.

10. (Currently amended)   The method of claim 7, further comprising

updating the reference group; ~~in such a way to calculate~~

calculating a difference values of ~~the~~ a start positions and ~~the~~ an end positions ~~of~~ for each ~~genetic~~ sequence information in the updated reference group; ~~which is commonly present on individual versions of the genome sequence~~ and

select~~ing~~ ~~genetic~~ sequence information in which the calculated difference value~~s are~~ is within a predetermined range.

11. (Currently amended)   The method of claim 7, wherein determining the location of the target genetic information comprises:

calculating a difference values of ~~the~~ a start positions and ~~the~~ an end positions of a ~~genetic~~ sequence information obtained from the crosslink map, wherein the sequence information was excluded from the reference group; ~~based on the crosslink map~~ and

setting an estimation region for the location of the target ~~genetic information~~ sequence on the ~~latest~~ genome sequence based on the calculated difference values; and

determining the location of the target ~~genetic information~~ sequence in the estimation region of the ~~latest~~ genome sequence by a location shift corresponding to the calculated difference value~~s calculated with respect to~~ for the reference ~~genetic~~ sequence information.

12. (Currently amended)   A computer readable medium having embodied thereon a computer program for ~~a~~ the method of determining a location of a target sequence in a genome sequence of claim 7,

wherein the computer readable medium is not a carrier wave.~~designing a probes using heterogeneous genetic information, the method comprising:~~

~~creating a crosslink map having records according to the version of a genome sequence;~~

~~searching for the identifier and sequence information corresponding to target genetic information among the genetic information about the genome sequence in the crosslink map;~~

~~determining a reference group made up of reference genetic information which is contained in more than a predetermined number in an organism;~~

~~calculating difference values of the start positions and the end positions of the reference genetic information based on the crosslink map; and~~

~~determining the location of the target genetic information on the latest genome sequence by a location shift corresponding to the difference values.~~

13. (New) The method of claim 8, wherein the location of the target sequence is determined in the version of the genome sequence represented in the crosslink map which is the most recent version of the genome sequence.

14. (New)   The method of claim 7, further comprising
displaying the location of the target sequence in the genome sequence.